



SEQUENCE LISTING

SEQUENCE LISTING

<110> Logemann, Juergen
Jach, Guido
Gornhardt, Birgit
Mundy, John
Schell, Jeff
Eckes, Peter
Chet, Ilan

<120> Transgenic pathogen-resistant organism

<130> A29542-FWC-I-R 070037.0195

<140> US 09/729,141

<141> 2000-12-01

<150> 08/812,025

<151> 1997-03-06

<150> 08/457,797

<151> 1995-06-01

<150> 08/134,416

<151> 1993-10-08

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Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp
5 10 15 20

aat atc tgc aag tac aag gca cag agc ggc aag act gcc att tgc aag 153
 Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys
 25 30 35

tgc tat gtc aaa aag tgc ccc cgc gac ggc gcg aaa tgc gag ttt gac 201
 Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp
 40 45 50

agc tac aag ggg aag tgc tac tgc tagacggtga gcgaagggac gaagtaggct 255
 Ser Tyr Lys Gly Lys Cys Tyr Cys
 55 60

ggggggttatt ttactctgct 275

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 <213> Aspergillus giganteus

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 Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr
 20 25 30
 Ala Ile Cys Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys
 35 40 45
 Cys Glu Phe Asp Ser Tyr Lys Gly Lys Cys Tyr Cys
 50 55 60

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 <213> Aspergillus giganteus

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 20 25 30
 Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp Ser Tyr Lys Gly Lys
 35 40 45
 Cys Tyr Cys
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100-443887-100

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<221> mat_peptide
<222> (46)...(886)
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Gln	Ala	Ser	Ser	Ala	Asp	Tyr	Ala	Thr	Phe	Ile	Ala	Gly	Ile	Arg	Asn	
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aag ctc cgc aac ccg gcg cac ttc tcc cac aac cgc ccc gtg ctg ccg 198
Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg Pro Val Leu Pro
40 45 50

ccg	gtc	gag	ccc	aac	gtc	ccg	ccg	agc	agg	tgg	ttc	cac	gtc	gtg	ctc	246
Pro	Val	Glu	Pro	Asn	Val	Pro	Pro	Ser	Arg	Trp	Phe	His	Val	Val	Leu	
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aag gcc tcg ccg acc agc gcc ggg ctc acg ctg gcc att cgg gcg gac 294
Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp

aac Asn 85	atc Ile	tac Tyr	ctg Leu	gag Glu	ggc Gly 90	ttc Phe	aag Lys	agc Ser	agc Ser	gac Asp 95	ggc Gly	acc Thr	tgg Trp	tgg Trp	gag Glu 100	342
ctc Leu	acc Thr	ccg Pro	ggc Gly	ctc Leu 105	atc Ile	ccc Pro	ggc Gly	gcc Ala	acc Thr 110	tac Tyr	gtc Val	ggg Gly	ttc Phe	ggc Gly 115	ggc Gly	390
acc Thr	tac Tyr	cgc Arg	gac Asp 120	ctc Leu	ctc Leu	ggc Gly	gac Asp	acc Thr 125	gac Asp	aag Lys	ctg Leu	acc Thr	aac Asn 130	gtc Val	gct Ala	438
ctc Leu	ggc Gly	cgg Arg 135	cag Gln	cag Gln	ctg Leu	gcg Ala	gac Asp 140	gcg Ala	gtg Val	acc Thr	gcc Ala	ctc Leu 145	cac His	ggg Gly	cgc Arg	486
acc Thr	aag Lys 150	gcc Ala	gac Asp	aag Lys	ccg Pro	tcc Ser 155	ggc Gly	ccg Pro	aag Lys	cag Gln	cag Gln 160	cag Gln	gcg Ala	agg Arg	gag Glu	534
gcg Ala 165	gtg Val	acg Thr	acg Thr	ctg Leu	ctc Leu 170	ctc Leu	atg Met	gtg Val	aac Asn	gag Glu 175	gcc Ala	acg Thr	cgg Arg	ttc Phe	cag Gln 180	582
acg Thr	gtg Val	tct Ser	ggg Gly	ttc Phe 185	gtg Val	gcc Ala	ggg Gly	ttg Leu	ctg Leu 190	cac His	ccc Pro	aag Lys	gcg Ala	gtg Val 195	gag Glu	630
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tgg Trp	cag Gln	gac Asp 215	ctg Leu	tcc Ser	gcg Ala	gcg Ala	ctg Leu 220	ctg Leu	aag Lys	acg Thr	gac Asp 225	gtg Val 225	aag Lys	cct Pro	ccg Pro	726
ccg Pro	gga Gly 230	aag Lys	tcg Ser	cca Pro	gcg Ala	aag Lys 235	ttc Phe	gcg Ala	ccg Pro	atc Ile	gag Glu 240	aag Lys	atg Met	ggc Gly	gtg Val	774
agg Arg 245	acg Thr	gct Ala	gta Val	cag Gln	gcc Ala 250	gcc Ala	aac Asn	acg Thr	ctg Leu	ggg Gly 255	atc Ile	ctg Leu	ctg Leu	ttc Phe	gtg Val 260	822
gag Glu	gtg Val	ccg Pro	ggt Gly	ggg Gly 265	ttg Leu	acg Thr	gtg Val	gcc Ala	aag Lys 270	gcg Ala	ctg Leu	gag Glu	ctg Leu	ttc Phe 275	cat His	870

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 Ala Ser Gly Gly Lys
 280

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 <212> PRT
 <213> Hordeum vulgare

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 35 40 45
 Pro Val Leu Pro Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe
 50 55 60
 His Val Val Leu Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala
 65 70 75 80
 Ile Arg Ala Asp Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly
 85 90 95
 Thr Trp Trp Glu Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val
 100 105 110
 Gly Phe Gly Gly Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu
 115 120 125
 Thr Asn Val Ala Leu Gly Arg Gln Gln Leu Ala Asp Ala Val Thr Ala
 130 135 140
 Leu His Gly Arg Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln
 145 150 155 160
 Gln Ala Arg Glu Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala
 165 170 175
 Thr Arg Phe Gln Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro
 180 185 190
 Lys Ala Val Glu Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala
 195 200 205
 Gln Val Asn Gly Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp
 210 215 220
 Val Lys Pro Pro Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu
 225 230 235 240
 Lys Met Gly Val Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile
 245 250 255
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 acg gtg tcg ggg ttc gtg gcc ggg ctg ctg cac ccc aag gcg gtg gag 96
 Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu
 20 25 30
 aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg 144
 Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly
 35 40 45
 tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag ccc ccg 192
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
 50 55 60
 ccg gga aag tcg cca gcg aag ttc acg ccg atc gag aag atg ggc gtg 240
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
 65 70 75 80
 agg act gct gag cag gct gcg gct act ttg ggg atc ctg ctg ttc gtt 288

Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
85 90 95

gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttt cat 336
Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
100 105 110

gcg agt ggt ggg aaa taggtagttt tgcaggtata cctgcatggg taaatgtaaa 391
Ala Ser Gly Gly Lys
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35 40 45
Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
50 55 60
Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
65 70 75 80
Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
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Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
100 105 110
Ala Ser Gly Gly Lys
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<210> 8
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<212> DNA
<213> Serratia marcescens

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<223> ChiS gene from plasmid pLChis from E.coli A5187

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<222> (64)...(861)

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<223> potential polyadenylation site

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<221> sig_peptide

<222> (349)...(378)

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<222> (466)...(588)

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<221> mat_peptide

<222> (133)...(861)

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Met Arg Ser Leu Ala Val Val Val Ala Val Val Ala Thr Val Ala
1 5 10 15

atg gcc atc ggc acg gcg cgc ggc agc gtg tcc tcc atc gtc tcg cgc 156
Met Ala Ile Gly Thr Ala Arg Gly Ser Val Ser Ser Ile Val Ser Arg
20 25 30

gca cag ttt gac cgc atg ctt ctc cac cgc aac gac ggc gcc tgc cag 204
Ala Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln
35 40 45

gcc aag ggc ttc tac acc tac gac gcc ttc gtc gcc gcc gca gcc gcc 252
Ala Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Ala
50 55 60

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Val	Ala	Ala	Phe	Leu	Ala	Gln	Thr	Ser	His	Glu	Thr	Thr	Gly	Gly	Trp	
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Ala	Thr	Ala	Pro	Asp	Gly	Ala	Phe	Ala	Trp	Gly	Tyr	Cys	Phe	Lys	Gln	
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Glu	Arg	Gly	Ala	Ser	Ser	Asp	Tyr	Cys	Thr	Pro	Ser	Ala	Gln	Trp	Pro	
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Cys	Ala	Pro	Gly	Lys	Arg	Tyr	Tyr	Gly	Arg	Gly	Pro	Ile	Gln	Leu	Ser	
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His	Asn	Tyr	Asn	Tyr	Gly	Pro	Ala	Gly	Arg	Ala	Ile	Gly	Val	Asp	Leu	
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Leu	Ala	Asn	Pro	Asp	Leu	Val	Ala	Thr	Asp	Ala	Thr	Val	Gly	Phe	Lys	
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His	Ala	Val	Ile	Ala	Gly	Gln	Trp	Ser	Pro	Ser	Gly	Ala	Asp	Arg	Ala	
			195				200						205			
gca	ggc	cgg	gtg	ccc	ggg	ttt	ggt	gtg	atc	acc	aac	atc	atc	aac	ggc	732
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		210					215					220				
ggg	atc	gag	tgc	ggt	cac	ggg	cag	gac	agc	cgc	gtc	gcc	gat	cga	atc	780
Gly	Ile	Glu	Cys	Gly	His	Gly	Gln	Asp	Ser	Arg	Val	Ala	Asp	Arg	Ile	
	225					230					235					
ggg	ttt	tac	aag	cgc	tac	tgt	gac	atc	ctc	ggc	ggt	ggc	tac	ggc	aac	828
Gly	Phe	Tyr	Lys	Arg	Tyr	Cys	Asp	Ile	Leu	Gly	Val	Gly	Tyr	Gly	Asn	

Met 1	Arg	Ser	Leu	Ala 5	Val	Val	Val	Ala	Val 10	Val	Ala	Thr	Val	Ala 15	Met
Ala	Ile	Gly	Thr 20	Ala	Arg	Gly	Ser	Val 25	Ser	Ser	Ile	Val	Ser 30	Arg	Ala
Gln	Phe	Asp 35	Arg	Met	Leu	Leu	His 40	Arg	Asn	Asp	Gly	Ala 45	Cys	Gln	Ala
Lys 50	Gly	Phe	Tyr	Thr	Tyr	Asp 55	Ala	Phe	Val	Ala	Ala 60	Ala	Ala	Ala	Phe
Pro 65	Gly	Phe	Gly	Thr	Thr 70	Gly	Ser	Ala	Asp	Ala	Gln	Lys	Arg	Glu	Val 80
Ala	Ala	Phe	Leu	Ala 85	Gln	Thr	Ser	His	Glu 90	Thr	Thr	Gly	Gly	Trp 95	Ala
Thr	Ala	Pro	Asp 100	Gly	Ala	Phe	Ala	Trp 105	Gly	Tyr	Cys	Phe	Lys 110	Gln	Glu
Arg	Gly	Ala 115	Ser	Ser	Asp	Tyr	Cys 120	Thr	Pro	Ser	Ala	Gln	Trp	Pro	Cys
Ala	Pro 130	Gly	Lys	Arg	Tyr	Tyr 135	Gly	Arg	Gly	Pro	Ile	Gln	Leu	Ser	His
Asn 145	Tyr	Asn	Tyr	Gly	Pro 150	Ala	Gly	Arg	Ala	Ile 155	Gly	Val	Asp	Leu	Leu 160
Ala	Asn	Pro	Asp 165	Leu	Val	Ala	Thr	Asp	Ala 170	Thr	Val	Gly	Phe	Lys 175	Thr
Ala	Ile	Trp	Phe 180	Trp	Met	Thr	Ala	Gln 185	Pro	Pro	Lys	Pro	Ser 190	Ser	His
Ala	Val 195	Ile	Ala	Gly	Gln	Trp	Ser 200	Pro	Ser	Gly	Ala	Asp 205	Arg	Ala	Ala
Gly	Arg 210	Val	Pro	Gly	Phe	Gly 215	Val	Ile	Thr	Asn	Ile 220	Ile	Asn	Gly	Gly
Ile 225	Glu	Cys	Gly	His	Gly 230	Gln	Asp	Ser	Arg	Val 235	Ala	Asp	Arg	Ile	Gly 240
Phe	Tyr	Lys	Arg	Tyr 245	Cys	Asp	Ile	Leu	Gly 250	Val	Gly	Tyr	Gly	Asn 255	Asn
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 <222> (1)...(48)

<221> CDS
 <222> (49)...(1050)
 <223> preprotein of the glucanase GluG

<221> 3'UTR
 <222> (1051)...(1235)
 <223> partial, 14 nucleotides at the 3' end not shown

<221> polyA_signal
 <222> (1083)...(1088)
 <223> potential polyadenylation signal

<221> polyA_signal
 <222> (1210)...(1215)
 <223> potential polyadenylation signal

<221> mat_peptide
 <222> (133)...(1050)

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 Met Ala Arg
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aaa gat gtt gcc tcc atg ttt gca gtt gct ctc ttc att gga gca ttc 105
 Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe
 5 10 15

gct gct gtt cct acg agt gtg cag tcc atc ggc gta tgc tac ggc gtg 153
 Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val
 20 25 30 35

atc ggc aac aac ctc ccc tcc cgg agc gac gtg gtg cag ctc tac agg 201
 Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg
 40 45 50

tcc aag ggc atc aac ggc atg cgc atc tac ttc gcc gac ggg cag gcc 249
 Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala
 55 60 65

ctc	tcg	gcc	gtc	cgc	aac	tcc	ggc	atc	ggc	ctc	atc	ctc	gac	atc	ggc	297
Leu	Ser	Ala	Val	Arg	Asn	Ser	Gly	Ile	Gly	Leu	Ile	Leu	Asp	Ile	Gly	
		70					75					80				
aac	gac	cag	ctc	gcc	aac	atc	ggc	ggc	agc	acc	tcc	aac	gcg	gcc	tcc	345
Asn	Asp	Gln	Leu	Ala	Asn	Ile	Ala	Ala	Ser	Thr	Ser	Asn	Ala	Ala	Ser	
	85					90					95					
tgg	gtc	cag	aac	aac	gtg	cgg	ccc	tac	tac	cct	gcc	gtg	aac	atc	aag	393
Trp	Val	Gln	Asn	Asn	Val	Arg	Pro	Tyr	Tyr	Pro	Ala	Val	Asn	Ile	Lys	
100					105					110					115	
tac	atc	gcc	gcc	ggc	aac	gag	gtg	cag	ggc	ggc	gcc	acg	cag	agc	atc	441
Tyr	Ile	Ala	Ala	Gly	Asn	Glu	Val	Gln	Gly	Gly	Ala	Thr	Gln	Ser	Ile	
				120					125					130		
ctg	ccg	gcc	atg	cgc	aac	ctc	aac	gcg	gcc	ctc	tcc	gcg	gcg	ggg	ctc	489
Leu	Pro	Ala	Met	Arg	Asn	Leu	Asn	Ala	Ala	Leu	Ser	Ala	Ala	Gly	Leu	
			135					140					145			
ggc	gcc	atc	aag	gtg	tcc	acc	tcc	atc	cgg	ttc	gac	gag	gtg	gcc	aac	537
Gly	Ala	Ile	Lys	Val	Ser	Thr	Ser	Ile	Arg	Phe	Asp	Glu	Val	Ala	Asn	
		150					155					160				
tcc	ttc	ccg	ccc	tcc	gcc	ggc	gtg	ttc	aag	aac	gcc	tac	atg	acg	gac	585
Ser	Phe	Pro	Pro	Ser	Ala	Gly	Val	Phe	Lys	Asn	Ala	Tyr	Met	Thr	Asp	
	165					170					175					
gtg	gcc	cgg	ctc	ctg	gcg	agc	acc	ggc	gcg	ccg	ctg	ctc	gcc	aac	gtc	633
Val	Ala	Arg	Leu	Leu	Ala	Ser	Thr	Gly	Ala	Pro	Leu	Leu	Ala	Asn	Val	
180					185					190					195	
tac	ccc	tac	ttc	gcg	tac	cgt	gac	aac	ccc	ggg	agc	atc	agc	ctg	aac	681
Tyr	Pro	Tyr	Phe	Ala	Tyr	Arg	Asp	Asn	Pro	Gly	Ser	Ile	Ser	Leu	Asn	
				200					205					210		
tac	gcg	acg	ttc	cag	ccg	ggc	acc	acc	gtg	cgt	gac	cag	aac	aac	ggg	729
Tyr	Ala	Thr	Phe	Gln	Pro	Gly	Thr	Thr	Val	Arg	Asp	Gln	Asn	Asn	Gly	
			215					220					225			
ctg	acc	tac	acg	tcc	ctg	ttc	gac	gcg	atg	gtg	gac	gcc	gtg	tac	gcg	777
Leu	Thr	Tyr	Thr	Ser	Leu	Phe	Asp	Ala	Met	Val	Asp	Ala	Val	Tyr	Ala	
			230				235					240				
gcg	ctg	gag	aag	gcc	ggc	gcg	ccg	gcg	gtg	aag	gtg	gtg	gtg	tcg	gag	825
Ala	Leu	Glu	Lys	Ala	Gly	Ala	Pro	Ala	Val	Lys	Val	Val	Val	Ser	Glu	
	245					250					255					
agc	ggg	tgg	ccg	tcg	gcg	ggc	ggg	ttt	gcg	gcg	tcg	gcc	ggc	aat	gcg	873

Ser Gly Trp Pro Ser Ala Gly Gly Phe Ala Ala Ser Ala Gly Asn Ala
260 265 270 275

cgg acg tac aac cag ggg ctg atc aac cac gtc ggc ggg ggc acg ccc 921
Arg Thr Tyr Asn Gln Gly Leu Ile Asn His Val Gly Gly Gly Thr Pro
280 285 290

aag aag cgg gag gcg ctg gag acg tac atc ttc gcc atg ttc aac gag 969
Lys Lys Arg Glu Ala Leu Glu Thr Tyr Ile Phe Ala Met Phe Asn Glu
295 300 305

aac cag aag acc ggg gac gcc acg gag agg agc ttc ggg ctc ttc aac 1017
Asn Gln Lys Thr Gly Asp Ala Thr Glu Arg Ser Phe Gly Leu Phe Asn
310 315 320

ccg gac aag tcg ccg gca tac aac atc cag ttc tagtacgtgt agctacctag 1070
Pro Asp Lys Ser Pro Ala Tyr Asn Ile Gln Phe
325 330

ctcacatacc taaataaata agctgcacgt acgtacgtaa tgcggcatcc aagtgtaacg 1130
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gatacatcat catggtatga ataaaagata tggaagatgt tatga 1235

<210> 12

<211> 334

<212> PRT

<213> Hordeum vulgare

<400> 12

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Tyr	Gly	Val	Ile	Gly	Asn	Asn	Leu	Pro	Ser	Arg	Ser	Asp	Val	Val	Gln
		35					40					45			
Leu	Tyr	Arg	Ser	Lys	Gly	Ile	Asn	Gly	Met	Arg	Ile	Tyr	Phe	Ala	Asp
	50					55					60				
Gly	Gln	Ala	Leu	Ser	Ala	Val	Arg	Asn	Ser	Gly	Ile	Gly	Leu	Ile	Leu
65					70					75					80
Asp	Ile	Gly	Asn	Asp	Gln	Leu	Ala	Asn	Ile	Ala	Ala	Ser	Thr	Ser	Asn
			85						90					95	
Ala	Ala	Ser	Trp	Val	Gln	Asn	Asn	Val	Arg	Pro	Tyr	Tyr	Pro	Ala	Val
			100					105					110		
Asn	Ile	Lys	Tyr	Ile	Ala	Ala	Gly	Asn	Glu	Val	Gln	Gly	Gly	Ala	Thr
		115					120					125			
Gln	Ser	Ile	Leu	Pro	Ala	Met	Arg	Asn	Leu	Asn	Ala	Ala	Leu	Ser	Ala
		130				135					140				
Ala	Gly	Leu	Gly	Ala	Ile	Lys	Val	Ser	Thr	Ser	Ile	Arg	Phe	Asp	Glu
145					150					155					160
Val	Ala	Asn	Ser	Phe	Pro	Pro	Ser	Ala	Gly	Val	Phe	Lys	Asn	Ala	Tyr

